0420
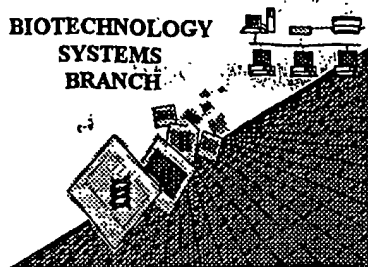
BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: *09/834,229*

Source: *OIPE*

Date Processed by STIC: *4/30/2001*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:
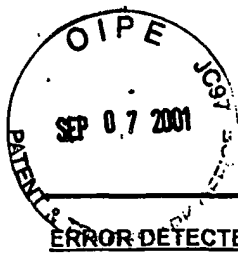
Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be downloaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

ERROR DETECTED   SUGGESTED   CORRECTION   SERIAL NUMBER: _09/834229_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 ✓ Variable Length
Sequence(s) _3_ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s)

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 ✓ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

OIPE

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229   TIME: 11:03:16

TP 1-3

Does Not Comply
Corrected Diskette Needed

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

```
   3 <110> APPLICANT: Efendic, Suad
   5 <120> TITLE OF INVENTION: USE OF GLP-1 OR ANALOGS IN TREATMENT OF MYOCARDIAL INFARCTION
   7 <130> FILE REFERENCE: X-10822A
   9 <140> CURRENT APPLICATION NUMBER: US/09/834,229
   9 <141> CURRENT FILING DATE: 2001-04-12
   9 <150> PRIOR APPLICATION NUMBER: US 60/024,980
  10 <151> PRIOR FILING DATE: 1996-08-30
  12 <150> PRIOR APPLICATION NUMBER: US 08/915,918
  13 <151> PRIOR FILING DATE: 1997-08-21
  15 <160> NUMBER OF SEQ ID NOS: 6
  17 <170> SOFTWARE: PatentIn version 3.0
  19 <210> SEQ ID NO: 1
  20 <211> LENGTH: 31
  21 <212> TYPE: PRT
  22 <213> ORGANISM: Homo sapiens
  24 <400> SEQUENCE: 1
  26 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
  27 1               5                   10                  15
  29 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Gly
  30              20                  25                  30
  32 <210> SEQ ID NO: 2
  33 <211> LENGTH: 31
  34 <212> TYPE: PRT
  35 <213> ORGANISM: Artificial
  37 <220> FEATURE:
  38 <223> OTHER INFORMATION: synthetic construct
  40 <220> FEATURE:
  41 <221> NAME/KEY: VARIANT
  42 <222> LOCATION: (1)..(1)
  43 <223> OTHER INFORMATION. Xaa at position 1 is L-histidine, D-histidine, desamino-histidine
  44        , 2-amino-histidine, B-hydroxy-histidine, homohistidine, alpha-fl
  45        uoromethyl-histidine, and aplpha-methyl-histidine
  48 <220> FEATURE:
  49 <221> NAME/KEY: VARIANT
  50 <222> LOCATION: (2)..(2)
  51 <223> OTHER INFORMATION: Xaa at position 2 is Ala, Gly, Val, Thr, Ile, and alpha-methyl Al
  55 <220> FEATURE:
  56 <221> NAME/KEY: VARIANT
  57 <222> LOCATION: (15)..(15)
  58 <223> OTHER INFORMATION: Xaa at position 15 is Glu, Gln, Ala, Thr, Ser, and Gly
  61 <220> FEATURE:
  62 <221> NAME/KEY: VARIANT
  63 <222> LOCATION: (21)..(21)
  64 <223> OTHER INFORMATION: Xaa at position 21 is Glu, Gln, Ala, Thr, Ser, and Gly
  67 <220> FEATURE:
  68 <221> NAME/KEY: VARIANT
  69 <222> LOCATION: (31)..(31)
```

see item 11 on Error Summary Sheet

(see item 3 on Error Summary Sheet
(line exceeds 72 characters)

←insert

Ala?

```
                RAW SEQUENCE LISTING              DATE: 04/30/2001
                PATENT APPLICATION: US/09/834,229  TIME: 11:03:17

                Input Set : A:\X-10822A_US Sequence Listing.txt
                Output Set: N:\CRF3\04302001\I834229.raw
```
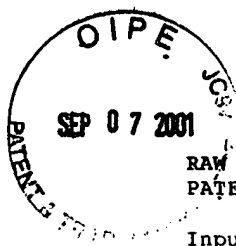
(handwritten, top right) Xaa can only represent a single amino acid, nothing else

```
        70 <223> OTHER INFORMATION: Xaa at position 31 is (NH2) and Gly-OH
        73 <400> SEQUENCE: 2
W-->    75 Xaa Xaa Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Xaa Gly
        76 1           5             10              15
W-->    78 Gln Ala Ala Lys Xaa Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
        79         20          25              30
        81 <210> SEQ ID NO: 3
        82 <211> LENGTH: 28
        83 <212> TYPE: PRT
C-->    84 <213> ORGANISM: Artificial    see item 11
        86 <220> FEATURE:
        87 <223> OTHER INFORMATION: synthetic construct
        89 <220> FEATURE:
        90 <221> NAME/KEY: VARIANT
        91 <222> LOCATION: (28)..(28)
        92 <223> OTHER INFORMATION: Xaa at position 28 is Lys and Lys-Gly
        95 <400> SEQUENCE: 3
        97 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
        98 1           5             10              15
W-->   100 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Xaa
       101         20          25
       103 <210> SEQ ID NO: 4
       104 <211> LENGTH: 30
       105 <212> TYPE: PRT
C-->   106 <213> ORGANISM: Artificial    item 11
       108 <220> FEATURE:
       109 <223> OTHER INFORMATION: synthetic construct
       111 <220> FEATURE:
       112 <221> NAME/KEY: VARIANT
       113 <222> LOCATION: (19)..(19)
       114 <223> OTHER INFORMATION: Xaa at position 19 is Lys or Arg
       117 <220> FEATURE:
       118 <221> NAME/KEY: VARIANT
       119 <222> LOCATION: (30)..(30)
       120 <223> OTHER INFORMATION: Xaa at position 30 is Gly-OH or (NH2)
       123 <400> SEQUENCE: 4
       125 Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly Gln
       126 1           5             10              15
W-->   128 Ala Ala Xaa Glu Phe Ile Ala Trp Leu Val Lys Gly Arg Xaa
       129         20          25              30
       131 <210> SEQ ID NO: 5
       132 <211> LENGTH: 30
       133 <212> TYPE: PRT
C-->   134 <213> ORGANISM: Artificial    item 11
       136 <220> FEATURE:
       137 <223> OTHER INFORMATION: synthetic construct
       139 <400> SEQUENCE: 5
       141 His Ala Glu Gly Thr Phe Thr Ser Asp Val Ser Ser Tyr Leu Glu Gly
       142 1           5             10              15
```

(handwritten, middle right) Xaa can only represent a single amino acid. Variable length is not acceptable — see item 6 on Error Summary Sheet

(handwritten, lower right) invalid use of Xaa

RAW SEQUENCE LISTING   DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229   TIME: 11:03:17

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

```
144 Gln Ala Ala Lys Glu Phe Ile Ala Trp Leu Val Lys Gly Arg
145             20              25          30
147 <210> SEQ ID NO: 6
148 <211> LENGTH: 4
149 <212> TYPE: PRT
150 <213> ORGANISM: Artificial
152 <220> FEATURE:
153 <223> OTHER INFORMATION: synthetic construct
155 <400> SEQUENCE: 6
157 Ser Arg Arg Gln
158 1
```

C--> *(handwritten annotation: "num 11")*

VERIFICATION SUMMARY   DATE: 04/30/2001
PATENT APPLICATION: US/09/834,229   TIME: 11:03:18

Input Set : A:\X-10822A_US Sequence Listing.txt
Output Set: N:\CRF3\04302001\I834229.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:35 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:75 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:78 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2
L:84 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:106 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:134 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:150 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:6